

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: August 4, 2003, 15:46:02 ; Search time 18 Seconds
(without alignments)
578.248 Million cell updates/sec

Title: US-09-931-836-2
Perfect score: 1367

Sequence: 1 MLWRLIYQQLALLFFLPFC.....LHGHDQRFSTFAGFLLFETK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA; *
1: /ccn2_6_ptodata/1/iaa/5A_COMB.pep:
2: /ccn2_6_ptodata/1/iaa/5B_COMB.pep:
3: /ccn2_6_ptodata/1/iaa/6A_COMB.pep:
4: /ccn2_6_ptodata/1/iaa/6B_COMB.pep:
5: /ccn2_6_ptodata/1/iaa/PCUTUS_Comb.pep:
6: /ccn2_6_ptodata/1/iaa/backfiles1..pep:*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	246	4 US-09-552-225A-2	Sequence 2, Appli
2	1311	95.9	246	4 US-09-552-225A-2	Sequence 12, Appli
3	912	42.6	105	3 US-09-188-930-147	Sequence 147, Appli
4	582	42.6	105	3 US-09-188-930-280	Sequence 280, Appli
5	582	42.6	105	4 US-09-312-283C-147	Sequence 147, Appli
6	582	42.6	105	4 US-09-312-283C-280	Sequence 280, Appli
7	319	23.3	285	4 US-09-312-283C-382	Sequence 382, Appli
8	316	23.1	294	3 US-09-188-930-294	Sequence 294, Appli
9	316	23.1	294	4 US-09-312-283C-294	Sequence 294, Appli
10	296	21.7	260	4 US-09-487-847-198	Sequence 198, Appli
11	296	21.7	21	287	4 US-09-487-349
12	294	21.5	247	2 US-09-463-911-2	Sequence 349, Appli
13	294	21.5	247	4 US-09-776-916-4	Sequence 2, Appli
14	294	21.5	247	4 US-09-509-517-4	Sequence 4, Appli
15	293.5	21.5	231	4 US-09-530-123-2	Sequence 4, Appli
16	293.5	21.5	244	3 US-08-463-911-7	Sequence 2, Appli
17	293.5	21.5	244	3 US-09-140-814-3	Sequence 7, Appli
18	293.5	21.5	244	4 US-09-336-336-20	Sequence 3, Appli
19	293.5	21.5	244	4 US-09-330-123-1	Sequence 20, Appli
20	293.5	21.5	244	4 US-09-586-938B-3	Sequence 1, Appli
21	293.5	21.5	244	4 US-09-911-176B-8	Sequence 3, Appli
22	293.5	21.5	244	4 US-09-552-225A-3	Sequence 48, Appli
23	293.5	21.5	244	4 US-09-619-740-51	Sequence 3, Appli
24	293.5	21.5	244	4 US-09-776-916-6	Sequence 6, Appli
25	293.5	21.5	244	4 US-09-909-547-6	Sequence 6, Appli
26	293.5	21.5	244	4 US-09-569-852B-6	Sequence 6, Appli
27	293	21.4	247	4 US-09-776-976-2	Sequence 2, Appli

RESULT 2
US-09-552-225A-12
; Sequence 12, Application US-09552225A
; Patent No. 6521233

ALIGNMENTS					
RESULT 1 US-09-552-225A-2					
Sequence 2, Application US-09552225A					
; Patent No. 6521233					
GENERAL INFORMATION:					
; APPLICANT: Piddington, Christopher S.					
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG 2 ACROP3					
; FILE REFERENCE: 99-09					
; CURRENT APPLICATION NUMBER: US-09-552-225A					
; CURRENT FILING DATE: 2000-04-19					
; PRIOR APPLICATION NUMBER: 60/130,199					
; NUMBER OF SEQ ID NOS: 20					
; SOFTWARE: FastSeq for Windows Version 3.0					
; SEQ ID NO: 2					
; LENGTH: 246					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-552-225A-2					
Query Match					
Best Local Similarity 100.0%; Pred. No. 6, 6e-130;					
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 MLWRLIYQQLALLFFLPFC.....LHGHDQRFSTFAGFLLFETK 246					
Db 1 MLWRLIYQQLALLFFLPFC.....LHGHDQRFSTFAGFLLFETK 246					
QY 1 MLWRLIYQQLALLFFLPFC.....LHGHDQRFSTFAGFLLFETK 246					
Db 1 MLWRLIYQQLALLFFLPFC.....LHGHDQRFSTFAGFLLFETK 246					
QY 61 PPGIPGNHGNNGNATCHEAKGEKGDKDGLGPRGRQHQGPKGKIPPELQIAF 60					
Db 61 PPGIPGNHGNNGNATCHEAKGEKGDKDGLGPRGRQHQGPKGKIPPELQIAF 60					
QY 61 YLMHNGNTVFSYNSYEMKGKSQTSSNHAVLKLAKGDEWLNGALHGDIHQRFSTFAGF 240					
Db 61 YLMHNGNTVFSYNSYEMKGKSQTSSNHAVLKLAKGDEWLNGALHGDIHQRFSTFAGF 240					
QY 121 MASLATHFSNQNSGIIFSVEVNIGNIGNFDMTGREGAPSVVYFFFSSMAMKHEDVEVYV 180					
Db 121 MASLATHFSNQNSGIIFSVEVNIGNIGNFDMTGREGAPSVVYFFFSSMAMKHEDVEVYV 180					
QY 181 YLMHNGNTVFSYNSYEMKGKSQTSSNHAVLKLAKGDEWLNGALHGDIHQRFSTFAGF 240					
Db 181 YLMHNGNTVFSYNSYEMKGKSQTSSNHAVLKLAKGDEWLNGALHGDIHQRFSTFAGF 240					
QY 241 LLFETK 246					
Db 241 LLFETK 246					